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Aphids are major pests of plants in temperate regions, especially by vectoring plant pathogens. Their success as crop pests principally arises from two characteristics: (1) their phenomenal reproductive rates by parthenogenesis during spring and summer and (2) their obligatory symbiotic bacteria *Buchnera aphidicola*, which provide aphids with essential amino acids lacking in their diet and contribute to aphids development and reproduction. Both pea aphid and *Buchnera* genomes have been recently sequenced and annotated, bringing this model of symbiosis to full genomic status. The availability of genomic data and tools allows the implementation of novel functional genomics research approaches to study the molecular mechanisms underlying embryo development in a parthenogenetic and symbiotic model organism. Using an oligonucleotides microarray, developed in collaboration with NimbleGen and including 24011 genes, we analysed the pea aphid transcriptome profiles at different embryonic and larval stages. Data were analysed using a linear ANOVA model and specific contrasts were applied, controlling the residual variance fluctuation, as well as the false discovery rate (R library limma). The analysis identified differentially expressed genes during embryo development using the following comparisons: i) early versus intermediate embryos, ii) intermediate versus late embryos and iii) late embryos versus early larval stages. We focused on the characterization of developmental and metabolic genes. This analysis, coupled with HPLC data on amino acids content obtained in the embryonic and larval stages, highlight an important role of aromatic amino acids biosynthetic genes at critical stage switches in pea aphid development.